UniProtKB/TrEMBL entry O84627

Entry information

Entry name	**O84627_CHLTR**
Primary accession number	**O84627**
Secondary accession numbers	None
Integrated into TrEMBL on	November 1, 1998
Sequence was last modified on	November 1, 1998 (Sequence version 1)
Annotations were last modified on	October 31, 2006 (Entry version 24)

Name and origin of the protein

Protein name	**CHLPN 76kDa Homolog**
Synonyms	None
Gene name	OrderedLocusNames: CT_622
From	Chlamydia trachomatis [TaxID: 813] [HAMAP proteome]
Taxonomy	Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.

References

[1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=D/UW-3/Cx;
DOI=10.1126/science.282.5389.754; PubMed=9784136
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V., Davis R.W.;
"Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.";
Science 282:754-759(1998).

Comments

Copyright

Cross-references

Sequence databases		
EMBL	AE001273; AAC68226.1; -; Genomic_DNA.	
PIR	G71490; G71490.	
2D gel databases		
PHCI-2DPAGE	O84627; -.	
Genome annotation databases		
GenomeReviews	AE001273_GR; CT_622.	
KEGG	ctr:CT622; -.	
Other		
Implicit links to	CMR; ProDom; HOGENOM; ModBase; UniRef.	

Keywords

Complete proteome.

Features

None

Sequence information

Length: **647 AA**
Molecular weight: **68526 Da**
CRC64: **C0D14C2D744736625** [This is a checksum on the sequence]

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         10         20         30         40         50         60
MESGPESVSS NQSSMNPIIN GQIASNSETK ESTKESEASP SASSSVSSWS FLSSAKHLALI
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          70         80         90        100        110        120
SLRDAILNKN SSFTDSLSQL EASTSTSTVT RVAARDYNEA KSNFDTAKSG LENATTIAEY

         130        140        150        160        170        180
ETKMADLMAA LQDMERLAKQ KAEVTRIKEA LQEKQEVIDK LNQLVKLEKQ NQTLKETLIT

         190        200        210        220        230        240
TDSADQIPAI NSQLEINKNS ADQIIKDLEG QNISYEAVLT NAGEVIKASS EAGIKLGQAL

         250        260        270        280        290        300
QSIVDAGDQS QAAVLQAQQN NSPDNIAATK KLIDAAETKV NELKQEHTGL TDSPLVKKAE

         310        320        330        340        350        360
EQISQAQKDI QEIKPSGSDI PIVGPSGSAA SAGSAVGALK SSNNSGRISL LLDDVDNEMA

         370        380        390        400        410        420
AIAMQGFRSM IEQFNVNNPA TAKELQAMEA QLTAMSDQLV GADGELPAEI QAIKDALAQA

         430        440        450        460        470        480
LKQPSTDGLA TAMGQVAFAA AKVGGGSAGT AGTVQMNVKQ LYKTAFSSTS SSSYAAALSD

         490        500        510        520        530        540
GYSAYKTLNS LYSESRSGVQ SAISQTANPA LSRSVSRSGI ESQGRSADAS QRAAETIVRD

         550        560        570        580        590        600
SQTLGDVYSR LQVLDSLMST IVSNPQVNQE EIMQKLTASI SKAPQFGYPA VQNSADSLQK

         610        620        630        640
FAAQLEREFV DGERSLAESR ENAFRKQPAF IQQVLVNIAS LFSGYLS
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